

[illegible]

Exon-Intron Boundary Sequences of the Human alpha-7 nAChR Subunit Gene

Exon Number	Exon length(bp)	cDNA position	splice acceptor	flanking exon sequence	splice donor	Intron number	Intron Size approximate (Kb)
1	55	1-55		...CTG CAC G	GTAAAGCCAC	1	0.3
2	140	56-195	TCTCCTTAAG	TG TCC.....GAC GTG	GTGAGTCCCG	2	Unknown
3	45	196-240	TTTTTTGAAG	GAT GAG.....CAA ATG	GTAAGTTAAG	3	9.0
4	110	241-350	TGTGTGTCCAG	TCT TGG.....AAC AG	GTAAGCATAT	4	Unknown
5	80	351-430	CTGTTTCTAG	T GCT GAT.....CCT CCA G	GTAAGCTGCA	5	4.0
6	168	431-598	ACCCACACAG	GC ATA.....CTA GTG G	GTAAGCCATG	6	1.0
7	195	599-793	CCCTATGGAG	GA ATC.....TCC CTG G	GTAAGCGCCC	7	1.0
8	87	794-880	TATGTTTTAG	GG ATA.....TTG ATA G	GTAAGGCAAG	8	3.5
9	110	881-990	CTCTCCACAG	CC CAG.....AAG TGG	GTACGTTTCT	9	5.0
10	519	991-1509	GTCTCCCCAG	ACC AGA...			

FIGURE 2

TABLE 2
Sequence Variants Identified in Full-Length and Duplicated Genomic Clones

DNA	EXONS CONT.	EXON 6 +/- 497-498		EXON 7 654		EXON 7 690		EXON 10 1269		EXON 10 1335		L76630
CHR15 HYBRID	5-10 1-10	+TG	-TG	C/T		G/A		C/C		C/C		6GT 8GT
YAC												
D-948a10	5-10		-TG		T		A		C			6GT
D-853b12	6-10		-TG		T		A		C			6GT
D/F 969b11	5-10 1-10	+TG	-TG	C/T		G/A		C/T		C/C		6GT 8GT
F-134h10	1-10	+TG				G		C		C		8GT
F-776a12	1-10	+TG				G		C		C		8GT
F-791e6	1-10	+TG				G		C		C		8GT
F-811b6	1-10	+TG				G		C		C		8GT
F-953g6	1-10	+TG				G		C		C		8GT
F-859c11	1-10	+TG				G		C		C		8GT
F-810f11	1-10	+TG				G		C		C		8GT
F-801e1	1-10	+TG				G		C		C		8GT
BAC												
F-467o18	1-10	+TG				G		C			T	8GT

DNA	Control #	EXON 6 +/- 497-498			EXON 7 654			EXON 7 690			EXON 10 1269			EXON 10 1335		
Control Genomic DNA	43	+/+	+/+	-/-	C/C	C/T	T/T	G/G	G/A	A/A	C/C	C/T	T/T	C/C	C/T	T/T
		10	33	0	5	38	0	0	43	0	6	36	1	24	19	0

FIGURE 3

TABLE 3
Expression Analysis of Sequence Variants

Subj	Bases 497-498			Base 654			Base 690			Base 933			Base 1296			Base 1335		
	DNA	1-10 cDNA	5-10 cDNA	DNA	1-10 cDNA	5-10 cDNA	DNA	1-10 cDNA	5-10 cDNA	DNA	1-10 cDNA	5-10 cDNA	DNA	1-10 cDNA	5-10 cDNA	DNA	1-10 cDNA	5-10 cDNA
SL061	+/-	+	+/-	CT	C	CT	GA	G	GA	G	G	G	CT	CT	CT	C	C	C
SL084	+	+	+	C	C	C	GA	G	GA	G	G	G	CT	C	CT	C	C	C
SL111	+/-	+	+/-	CT	C	CT	GA	G	GA	G	G	G	CT	CT	CT	CT	CT	CT
SL097	+	+	+	CT	C	CT	GA	G	GA	G	G	G	CT	C	CT	C	C	C
SL089	+	+	+	C	C	C	GA	GA	GA	GA	GA	GA	CT	CT	CT	C	C	C
SHSY	+/-	+	+/-	CT	C	CT	GA	GA	GA	GA	GA	GA	C	C	C	C	C	C

— 222 —

THE

FIGURE 5

[illegible]

FIGURE 6

EXON D 297bp	1	CAGGCCGCCA	CATAGCTCCC	GCCAAGTCCT	CGGTGCCCCT	TGCCATTTTC	CAGCCGCGTC	CCACGAGGGT
		CACGGCGGCG	GGGAGAGGTG	GAGCCGCGAG	AGCTCGGCCG	GGGGCCCCCG	CTGGTGGCCG	CGGCCATGAC
		AGCGGCTCGG	GACTGGCTCC	TTTTCCGCGC	CCCTCCCGCC	GGAGGTGAGG	GGAAGATGTC	CATGTCAGGG
		TTCAAGGCCA	AACCGAAGTT	ACTGGCCTCT	ATCTTCCAGG	AGAACCAGGA	GCCACAGCCG	CGGCTCACGC
		CCCACCGCAA	CATTAAGgtg	agtcgcc.....				
EXON C 125bp	297							
	298ctc	atttcagATT	ACAAGTGGAC	ACCTGAGTCA	GCAGGACCTG	GAATCCCAGA	TGAGAGAGCT
		TATCTACACG	ACTCAGATCT	TGTTGTCACC	CCCATTATTG	ACAATCCAAA	GGTGCAGAAA	GCACTCTGAC
		AAgtgagttg	ta.....					
EXON B 64bp	422							
	423	..ttaaccac	agATAATGAA	ACAACCACCA	TCGGTTAAAT	TTGATGCAAA	AATATTGCAT	CTACCAGCAT
		TTTCAGgtag	gatcat.....					
EXON A 47bp	486							
	487ttta	ttctagTTCC	AATTGCTAAT	CCAGCATTTG	TGGATAGCTG	CAAAC TGCGA	TATgtaagta
EXON 5 80bp		aca.....						533
	534	...ctgtttc	tagTGCTGAT	GAGCGCTTTG	ACGCCACATT	CCACACTAAC	GTGTTGGTGA	ATTCTTCTGG
			GCATTGCCAG	TACCTGCCTC	CAGgtaagctgca.....			
EXON 6 27bp	613							
	614accaca	cagGCATATT	CAAGAGTTCC	TGCTACATCG			
	640							

FIGURE 7

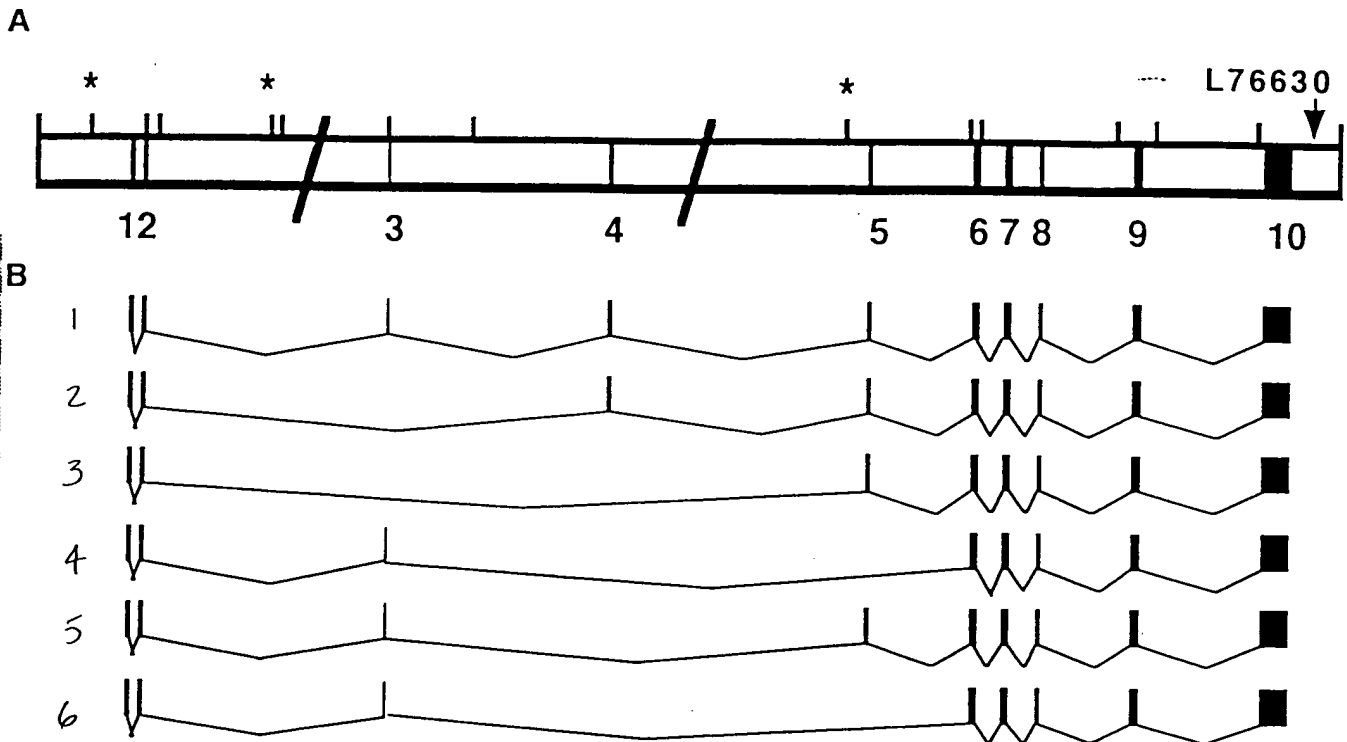


FIGURE 8

1 agaacgcaag ggagaggtag agcctggcct tgggcagccc ctggcctggc cagaggcgcg
61 aggccgagag cccgctcggg ggagactggg ggtggagggtg cccggagcgt acccagcgcc
121 gggagtacct cccgctcaca cctcgggctg cagttccctg ggtggccgcc gagacgtgg
181 cccgggctgg agggatggcg gggcgggggac gggggcgggg gcggggctcg tcacgtggag
241 aggcgcgcgg gggcgggcgg ggcgggggcg cgcgcccgcc tcctaaagg cgcgcgagcc
301 gagcggcgag gtgcctctgt ggccgcaggc gcaggcccg gcgacagccg agacgtggag
361 cgcgccggct cgctgcagct ccgggactca ac

FIGURE 9

1 agccctttcc caggcggtag cggggggcagt ggtgctgttg ccttttaaa ctgcggcttg
61 acggggagccg cgcctcctgt cgggtggagtc ggttataaag ggagcagccc cgcaggcccg
121 cacatagctc ccgccaagtc ctcggtgcc cttgccattt tccagcccg ctcccacgag
181 ggtcacggcg gcgggggagag gtggagccgc gagagctcgg ccggggggccc cgcttgggtg
241 ccgcggccat gacagcggct cgggactggc tcttttccg cgcccctccc gccggaggtg
301 aggggaagat gtccatgtca ggggtcaagg ccaaaccgaa gttactggcc tctatcttc
361 aggagaacca ggagccacag ccgcggctca cgccccaccg caacattaag attacaaagt
421 gacacctgag tcagcaggac ctggaatccc agatgagaga gcttatctac acgactcaga
481 tcttgtgtc acccccatta ttgacaatcc aaaggtgcag aaagcactct gacaattcca
541 attgctaate cagcatttgt gगतगctgc aaactgcgat attgctgatg agcgctttga
601 cgccacattc cacactaacg tgttggtgaa ttctctggg cattgccagt acctgcctcc
661 aggcataattc aagagttcct gctacatcg

FIGURE 10

1 caggccgcca catagctccc gccaatgctt cgggtgcccct tgccattttc cagccgcgct
61 cccacgaggg tcacggcggc ggggagaggt ggagccgcga gagctcggcc gggggccccg
121 cctggtggcc gcggccatga cagcggctcg ggactggctc cttttccgcg cccctccgc
181 cggaggtgag gggaagatgt ccatgtcagg gttcaaggcc aaaccgaagt tactggcctc
241 tatcttcag gagaaccagg agccacagcc gcggctcacg ccccaccgca acattaagat
301 tacaagtgga cacctgagtc agcaggacct ggaatcccag atgagagagc ttatctacac
361 gactcagatc ttgtgtcac cccattatt gacaatccaa aggtgcagaa agcactctga
421 caaataatga aacaaccacc atcgggtaaa ttgatgcaa aaatattgca tctaccagca
481 tttcagttc caattgctaa tccagcattt gtggatagct gcaaactgcg atattgctga
541 tgagcgcttt gacgccacat tccacactaa cgtgttggtg aattcttctg ggcattgcca
601 gtacctgcct ccaggcatat tcaagagttc ctgctacatc g

035513-10297